

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: MUKHERJEE, RANJAN

(ii) TITLE OF INVENTION: Human Peroxisome Proliferator Activated Receptor γ RECEIVED MAY 10 1995
CPDNIP 1200

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
(C) CITY: Suite 4700
(D) STATE: Los Angeles
(E) COUNTRY: California
(F) ZIP: U.S.A.
90071-2066

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/380,051
(B) FILING DATE: January 30, 1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Warburg, Richard J.
(B) REGISTRATION NUMBER: 32,327
(C) REFERENCE/DOCKET NUMBER: 210/100

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (213) 489-1600
(B) TELEFAX: (213) 955-0440
(C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCCGGA CCCTCAACAC CACTCCCTCT TAGCCAATAT TGTGCCTATT 50
 GCCATACTAG TCTTGCGGCC TGCAGAAGCAG CGGTGGCCTA GCCCTACTAG 100
 TCTCAATCTC CAACATATAT CGGCCTAGAC TACGTACATA ACCTAACACCT 150
 ACTCCAATGC TAAAACTAAT CGTCCCTTTT CTCAAACGAG AGTCAGCCTT 200
 TAACGAAATG ACCATGGTTG ACACAGAGAT GCCATTCTGG CCCACCAACT 250
 TTGGGATCAG CTCCGTGGAT CTCTCCGTAA TGGAAGACCA CTCCCACCTCC 300
 TTTGATATCA AGCCCTTCAC TACTGTTGAC TTCTCCAGCA TTTCTACTCC 350
 ACATTACGAA GACATTCCAT TCACAAGAAC AGATCCAGTG GTTGCAGATT 400
 ACAAGTATGA CCTGAAACTT CAAGAGTACC AAAGTGCAAT CAAAGTGGAG 450
 CCTGCATCTC CACCTTATTA TTCTGAGAAG ACTCAGCTCT ACAATAAGCC 500
 TCATGAAGAG CCTTCCAATC CCCTCATGGC AATTGAATGT CGTGTCTGTG 550
 GAGATAAAGC TTCTGGATT CACTATGGAG TTCATGCTTG TGAAGGATGC 600
 AAGGGTTTCT TCCGGAGAAC AATCAGATTG AAGCTTATCT ATGACAGATG 650
 TGATCTAAC TGTGGATCC ACAAAAAAAG TAGAAATAAA TGTCAGTACT 700
 GTCGGTTCA GAAATGCCTT GCAGTGGGA TGTCTCATAA TGCCATCAGG 750
 TTTGGGCGGA TGCCACAGGC CGAGAAGGAG AAGCTGTTGG CGGAGATCTC 800
 CAGTGATATC GACCAGCTGA ATCCAGAGTC CGCTGACCTC CGGGCCCTGG 850
 CAAACATTT GTATGACTCA TACATAAAGT CCTTCCCGCT GACCAAAGCA 900
 AAGGCGAGGG CGATCTTGAC AGGAAAGACA ACAGACAAAT CACCATTCGT 950
 TATCTATGAC ATGAATTCT TAATGATGGG AGAAGATAAA ATCAAGTTCA 1000
 AACACATCAC CCCCTGCAG GAGCAGAGCA AAGAGGTGGC CATCCGCATC 1050
 TTTCAGGGCT GCCAGTTCG CTCCGTGGAG GCTGTGCAGG AGATCACAGA 1100
 GTATGCCAAA AGCATTCCCTG GTTTGTAAA TCTTGACTTG AACGACCAAG 1150

cont.

TAACCTCCCT CAAATATGGA GTCCACGAGA TCATTTACAC AATGCTGGCC 1200
TCCTTGATGA ATAAAGATGG GGTTCTCATA TCCGAGGGCC AAGGCTTCAT 1250
GACAAGGGAG TTTCTAAAGA GCCTGCGAAA GCCTTTGGT GACTTTATGG 1300
AGCCCAAGTT TGAGTTTGCT GTGAAGTTCA ATGCACTGGA ATTAGATGAC 1350
AGCGACTTGG CAATATTTAT TGCTGTCATT ATTCTCAGTG GAGACCGCCC 1400
AGGTTTGCTG AATGTGAAGC CCATTGAAGA CATTCAAGAC AACCTGCTAC 1450
AAGCCCTGGA GCTCCAGCTG AAGCTGAACC ACCCTGAGTC CTCACAGCTG 1500
TTTGCCAAGC TGCTCCAGAA AATGACAGAC CTCAGACAGA TTGTCACCGA 1550
ACACGTGCAG CTACTGCAGG TGATCAAGAA GACGGAGACA GACATGAGTC 1600
TTCACCCGCT CCTGCAGGAG ATCTACAAGG ACTTGTACTA G 1641

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 amino acids
(B) TYPE: amino acid
(C) STRANDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION : SEQ ID NO: 2

Met Leu Lys Leu Ile Val Pro Phe Leu Lys Arg Glu Ser Ala Phe
5 10 15

Asn Glu Met Thr Met Val Asp Thr Glu Met Pro Phe Trp Pro Thr
20 25 30

Asn Phe Gly Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp His
35 40 45

Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser
50 55 60

Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe Thr Arg Thr
65 70 75

Asp, Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu Gln Glu
80 85 90

Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr Tyr
 95 100 105
 Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser
 110 115 120
 Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala
 125 130 135
 Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly
 140 145 150
 Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
 155 160 165
 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln
 170 175 180
 Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
 185 190 195
 Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu
 200 205 210
 Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser
 215 220 225
 Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile
 230 235 240
 Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr
 245 250 255
 Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn
 260 265 270
 Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr
 275 280 285
 Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln
 290 295 300
 Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu
 305 310 315
 Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp
 320 325 330
 Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr
 335 340 345
 Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu
 350 355 360
 Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys
 365 370 375

A
wt.

Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys
380 385 390

Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
395 400 405

Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val
410 415 420

Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
425 430 435

Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala
440 445 450

Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu
455 460 465

His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met
470 475 480

Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
485 490

a
cont.